RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: _/0/563,896_____

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Date Processed by STIC: _____8/25/06____

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RAW SEQUENCE LISTING   DATE: 08/25/2006
PATENT APPLICATION: US/10/563,896   TIME: 12:09:06

Input Set : E:\seq_490051_402uspc.app.txt
Output Set: N:\CRF4\08252006\J563896.raw

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   3 <110> APPLICANT: TAKEDA, Junji
   4         HORIE, Kyoji
   6 <120> TITLE OF INVENTION: METHOD OF PREPARING TRANSGENIC ORGANISM WITH USE OF
METHYLATION
   7         AND SYTEM THEREFOR
   9 <130> FILE REFERENCE: 490051.402USPC
  11 <140> CURRENT APPLICATION NUMBER: US 10/563,896
C--> 12 <141> CURRENT FILING DATE: 2006-01-09
  14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/010090
  15 <151> PRIOR FILING DATE: 2004-07-08
  17 <160> NUMBER OF SEQ ID NOS: 76
  19 <170> SOFTWARE: PatentIn version 3.2
  21 <210> SEQ ID NO: 1
  22 <211> LENGTH: 1455
  23 <212> TYPE: DNA
  24 <213> ORGANISM: Tanichthys albonubes
  27 <220> FEATURE:
  28 <221> NAME/KEY: misc_feature
  29 <222> LOCATION: (1)..(1455)
  30 <223> OTHER INFORMATION: /note="Tc1-like transposon"
  32 <300> PUBLICATION INFORMATION:
  33 <308> DATABASE ACCESSION NO: L48685
  34 <309> DATABASE ENTRY DATE: 1996-05-31
  35 <313> RELEVANT RESIDUES: (1)..(1455)
  37 <400> SEQUENCE: 1
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  40 tacaccacaa atttcttgtt aacaaacaat agttttggca agtcagttag gacatctact     120
  42 ttgtgcatga cacaagtcat ttttccaaca attgtttaca gacagattat ttcacttata     180
  44 attcactgta tcacaattcc agtgggtcag aagtttacat acactaagtt gactgtgcct     240
  46 ttaaacagct tggaaaattc cagaaaatga tgtcatggct ttagaagctt ctgatagact     300
  48 aattgacatc atttgagtca attggaggtg tacctgtgga tgtatttcaa ggcctacctt     360
  50 caaacgcagt gcctctttgc ttgacataat gggaaaatca aaagaaatca gccaacacca     420
  52 tgggaccacg cagccgtcat accgctcagg aatgagacgc attctgtctc ctagagataa     480
  54 acatactgtg gtgcgaaaag tgcaaatcaa tcccagaacg acagcaaagg accttgtgaa     540
  56 gatgctggag aaaacaggta tgaatgtttc tatatccaca gtaaaaacga gtcctatatc     600
  58 gacataacct gaaaggccgc tcagcaagga agaagccact gctccaaaac cgccataaaa     660
  60 aagccagact acggtttgca actgcacatg gggacaaata tggtactttt ggagaaatg     720
  62 tcctctcttc tggtctgatg aaaaaaaaat agaactattt ggccataatg accatcgtta     780
  64 tgtttggagg aaaaaggggg agcttgcaag ccgaagatca ccatcccaag cgtgaagcac     840
  66 ggggggtggca gcatcatgtt gtgggggtgc tttgctgcag gagggactgg tgcacttcac     900
  68 aaaatagatg gcatcatgac aaaggaaaat tatgtggcta tattgaagca acatctcaag     960
  70 acatcagtca ggaagttcaa gcttggtcac aaatgggtct tccaaatgga caatgacctc    1020
  72 aagcatactt ccaaagttgt ggcaaaatgg cttaaggtca acaaagtcaa ggtattggag    1080
  74 tggccatcac aaagctctga cctcaatcct atagaaagga ggaatgagcc aaaattcacc    1140
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76 caacttattg tgggaagctt gtggaaggct actcgaaatg tttgacccaa gttaaacaat   1200
78 ttaaaggcaa tgctaccaaa tactaattga gtgtatgtta acttctgacc cactgggaat   1260
80 gtgatgaaag aaataaaagc tgaaatgaat cattctctct actattattc tgatatttca   1320
82 cattcttaaa ataaagtggt gatcctaact gaccttaaga cagggaatct ttactcggat   1380
84 taaatgtcag gaattgtgaa aaagtgagtt taaatgtatt tggctaaggt gtatgtaaac   1440
86 ttccgacttc aactg                                                      1455
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90 <211> LENGTH: 1023
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Sleeping Beauty transposase
98 <220> FEATURE:
99 <221> NAME/KEY: CDS
100 <222> LOCATION: (1)..(1023)
102 <220> FEATURE:
103 <221> NAME/KEY: misc_feature
104 <222> LOCATION: (1)..(1023)
105 <223> OTHER INFORMATION: Sleeping Beauty transposase
107 <400> SEQUENCE: 2
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109 Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Lys Ile Val
110 1               5                  10                  15
112 gac ctc cac aag tct ggt tca tcc ttg gga gca att tcc aaa cgc ctg       96
113 Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
114                 20                  25                  30
116 aaa gta cca cgt tca tct gta caa aca ata gta cgc aag tat aaa cac      144
117 Lys Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
118             35                  40                  45
120 cat ggg acc acg cag ccg tca tac cgc tca gga agg aga cgc gtt ctg      192
121 His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
122     50                  55                  60
124 tct cct aga gat gaa cgt act ttg gtg cga aaa gtg caa atc aat ccc      240
125 Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
126 65                  70                  75                  80
128 aga aca aca gca aag gac ctt gtg aag atg ctg gag gaa aca ggt aca      288
129 Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
130                 85                  90                  95
132 aaa gta tct ata tcc aca gta aaa cga gtc cta tat cga cat aac ctg      336
133 Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
134                 100                 105                 110
136 aaa ggc cgc tca gca agg aag aag cca ctg ctc caa aac cga cat aag      384
137 Lys Gly Arg Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
138             115                 120                 125
140 aaa gcc aga cta cgg ttt gca act gca cat ggg gac aaa gat cgt act      432
141 Lys Ala Arg Leu Arg Phe Ala Thr Ala His Gly Asp Lys Asp Arg Thr
142     130                 135                 140
144 ttt tgg aga aat gtc ctc tgg tct gat gaa aca aaa ata gaa ctg ttt      480
145 Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
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Input Set : E:\seq_490051_402uspc.app.txt
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146 145                   150                 155                 160
148 ggc cat aat gac cat cgt tat gtt tgg agg aag aag ggg gag gct tgc   528
149 Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
150                   165                 170                 175
152 aag ccg aag aac acc atc cca acc gtg aag cac ggg ggt ggc agc atc   576
153 Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
154                   180                 185                 190
156 atg ttg tgg ggg tgc ttt gct gca gga ggg act ggt gca ctt cac aaa   624
157 Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
158          195                 200                 205
160 ata gat ggc atc atg agg aag gaa aat tat gtg gat ata ttg aag caa   672
161 Ile Asp Gly Ile Met Arg Lys Glu Asn Tyr Val Asp Ile Leu Lys Gln
162      210                 215                 220
164 cat ctc aag aca tca gtc agg aag tta aag ctt ggt cgc aaa tgg gtc   720
165 His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
166 225                   230                 235                 240
168 ttc caa atg gac aat gac ccc aag cat act tcc aaa gtt gtg gca aaa   768
169 Phe Gln Met Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
170                   245                 250                 255
172 tgg ctt aag gac aac aaa gtc aag gta ttg gag tgg cca tca caa agc   816
173 Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
174          260                 265                 270
176 cct gac ctc aat cct ata gaa aat ttg tgg gca gaa ctg aaa aag cgt   864
177 Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
178          275                 280                 285
180 gtg cga gca agg agg cct aca aac ctg act cag tta cac cag ctc tgt   912
181 Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
182      290                 295                 300
184 cag gag gaa tgg gcc aaa att cac cca act tat tgt ggg aag ctt gtg   960
185 Gln Glu Glu Trp Ala Lys Ile His Pro Thr Tyr Cys Gly Lys Leu Val
186 305                   310                 315                 320
188 gaa ggc tac ccg aaa cgt ttg acc caa gtt aaa caa ttt aaa ggc aat   1008
189 Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
190          325                 330                 335
192 gct acc aaa tac tag                                                1023
193 Ala Thr Lys Tyr
194          340
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 340
199 <212> TYPE: PRT
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: Synthetic Construct
205 <400> SEQUENCE: 3
207 Met Gly Lys Ser Lys Glu Ile Ser Gln Asp Leu Arg Lys Lys Ile Val
208 1               5                   10                  15
211 Asp Leu His Lys Ser Gly Ser Ser Leu Gly Ala Ile Ser Lys Arg Leu
212          20                  25                  30
215 Lys Val Pro Arg Ser Ser Val Gln Thr Ile Val Arg Lys Tyr Lys His
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Input Set : **E:\seq_490051_402uspc.app.txt**
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216        35                    40                    45
219 His Gly Thr Thr Gln Pro Ser Tyr Arg Ser Gly Arg Arg Arg Val Leu
220     50                    55                    60
223 Ser Pro Arg Asp Glu Arg Thr Leu Val Arg Lys Val Gln Ile Asn Pro
224 65                    70                    75                    80
227 Arg Thr Thr Ala Lys Asp Leu Val Lys Met Leu Glu Glu Thr Gly Thr
228                     85                    90                    95
231 Lys Val Ser Ile Ser Thr Val Lys Arg Val Leu Tyr Arg His Asn Leu
232                 100                   105                   110
235 Lys Gly Arg Ser Ala Arg Lys Lys Pro Leu Leu Gln Asn Arg His Lys
236             115                   120                   125
239 Lys Ala Arg Leu Arg Phe Ala Thr Ala His Gly Asp Lys Asp Arg Thr
240       130                   135                   140
243 Phe Trp Arg Asn Val Leu Trp Ser Asp Glu Thr Lys Ile Glu Leu Phe
244 145                   150                   155                   160
247 Gly His Asn Asp His Arg Tyr Val Trp Arg Lys Lys Gly Glu Ala Cys
248                 165                   170                   175
251 Lys Pro Lys Asn Thr Ile Pro Thr Val Lys His Gly Gly Gly Ser Ile
252                 180                   185                   190
255 Met Leu Trp Gly Cys Phe Ala Ala Gly Gly Thr Gly Ala Leu His Lys
256             195                   200                   205
259 Ile Asp Gly Ile Met Arg Lys Glu Asn Tyr Val Asp Ile Leu Lys Gln
260       210                   215                   220
263 His Leu Lys Thr Ser Val Arg Lys Leu Lys Leu Gly Arg Lys Trp Val
264 225                   230                   235                   240
267 Phe Gln Met Asp Asn Asp Pro Lys His Thr Ser Lys Val Val Ala Lys
268                 245                   250                   255
271 Trp Leu Lys Asp Asn Lys Val Lys Val Leu Glu Trp Pro Ser Gln Ser
272             260                   265                   270
275 Pro Asp Leu Asn Pro Ile Glu Asn Leu Trp Ala Glu Leu Lys Lys Arg
276             275                   280                   285
279 Val Arg Ala Arg Arg Pro Thr Asn Leu Thr Gln Leu His Gln Leu Cys
280       290                   295                   300
283 Gln Glu Glu Trp Ala Lys Ile His Pro Thr Tyr Cys Gly Lys Leu Val
284 305                   310                   315                   320
287 Glu Gly Tyr Pro Lys Arg Leu Thr Gln Val Lys Gln Phe Lys Gly Asn
288             325                   330                   335
291 Ala Thr Lys Tyr
292             340
295 <210> SEQ ID NO: 4
296 <211> LENGTH: 26
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Left outside sequence
303 <400> SEQUENCE: 4
304 gttgaagtcg gaagtttaca cttagg                              26
307 <210> SEQ ID NO: 5
308 <211> LENGTH: 30
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        Input Set : E:\seq_490051_402uspc.app.txt
        Output Set: N:\CRF4\08252006\J563896.raw

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309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Left inside sequence
315 <400> SEQUENCE: 5
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319 <210> SEQ ID NO: 6
320 <211> LENGTH: 27
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence;
324 <220> FEATURE:
325 <223> OTHER INFORMATION: TgTP-1U
327 <400> SEQUENCE: 6
328 gaccgcttcc tcgtgcttta cggtatc                                   27
331 <210> SEQ ID NO: 7
332 <211> LENGTH: 30
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence;
336 <220> FEATURE:
337 <223> OTHER INFORMATION: TgTP-2L
339 <400> SEQUENCE: 7
340 acacaggaaa cagctatgac catgattacg                                30
343 <210> SEQ ID NO: 8
344 <211> LENGTH: 30
345 <212> TYPE: DNA
346 <213> ORGANISM: Artificial Sequence;
348 <220> FEATURE:
349 <223> OTHER INFORMATION: TgTP-2U
351 <400> SEQUENCE: 8
352 tctatcgcct tcttgacgag ttcttctgag                                30
355 <210> SEQ ID NO: 9
356 <211> LENGTH: 28
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial Sequence;
360 <220> FEATURE:
361 <223> OTHER INFORMATION: TgTP-3L
363 <400> SEQUENCE: 9
364 caagcgcgca attaaccctc actaaagg                                  28
367 <210> SEQ ID NO: 10
368 <211> LENGTH: 1610
369 <212> TYPE: DNA
370 <213> ORGANISM: Caenorhabditis elegans
373 <220> FEATURE:
374 <221> NAME/KEY: misc_feature
375 <222> LOCATION: (1)..(1610)
376 <223> OTHER INFORMATION: Transposon="Tc1"
378 <220> FEATURE:
379 <221> NAME/KEY: CDS
380 <222> LOCATION: (523)..(1344)
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/25/2006
PATENT APPLICATION: US/10/563,896   TIME: 12:09:07

Input Set : **E:\seq_490051_402uspc.app.txt**
Output Set: **N:\CRF4\08252006\J563896.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:64; N Pos. 13
Seq#:65; N Pos. 21

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43
Seq#:44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67
Seq#:68,69,70,71,72,73,74,75,76

VERIFICATION SUMMARY DATE: 08/25/2006
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:64 after pos.:0
L:2105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:0